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LATEST COVID-19 BIOSURVEILLANCE REPORT

Sequence result release: November 22 - December 1, 2023

VARIANT DISTRIBUTION OVER TIME

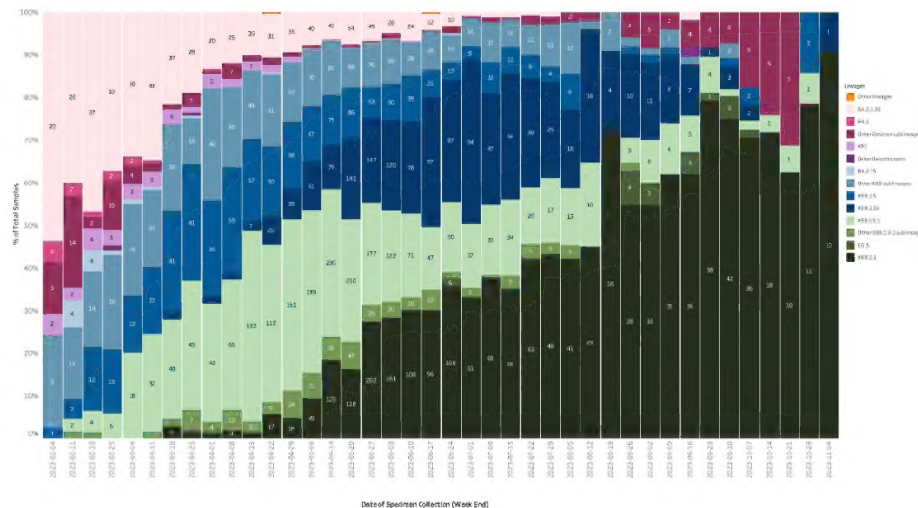


Figure 1. Samples sequenced from the Philippines, collected from February 2023 onwards.

Figure 1 above shows the proportion of variants sequenced by the University of the Philippines - Philippine Genome Center (UP-PGC) Main, Visayas, and Mindanao, Research Institute for Tropical Medicine (RITM), San Lazaro Hospital (SLH), Southern Philippines Medical Center (SPMC), Baguio General Hospital Medical Center (BGHMC), and Vicente Sotto Memorial Medical Center (VSMC) with collection dates from February 2023 onwards.

After the observed increase in the number and proportion of the Omicron subvariant BA.5 since July 2022, different Omicron subvariants under monitoring that were previously and are currently being flagged by the World Health Organization (WHO) or European Centre for Disease Prevention and Control (ECDC) (ie. BA.2.3.20, XBB and its sublineages) have been on a continuous uptrend starting September 2022. From October 2023 onwards, XBB and its sublineages were the most detected variants, comprising 82.61% of samples sequenced with assigned lineages. For the same period, XBB.2.3 was the most detected XBB sublineage comprising 87.37% of XBB cases sequenced.

Note that the graph above must be interpreted with caution due to sampling biases brought about by factors such as changes in testing protocols and other logistical issues. Moreover, as we continue sequencing samples, the proportion of each variant may vary over time.

WGS RESULTS released on November 22 - December 1, 2023

Table 1. Cumulative count and percentage of sequenced Omicron subvariants and their respective classification under the World Health Organization (WHO) and European Centre for Disease Prevention and Control (ECDC).

Lineage ^a	Count (Percent to Total) ^b	Classification	
		WHO As of November 21, 2023	ECDC As of December 1, 2023
XBB.1.5	877 (1.46%)	VOI	VOI
XBB.1.16	1,206 (2.01%)	VOI	N/A
EG.5	28 (0.05%)	VOI	VOI <i>Monitored under XBB.1.5-like + F456L^d</i>
BA.2.75	73 (0.12%)	N/A	VOI
XBB	8,571 (14.31%)	VUM	N/A
XBB.1.9.1	1,945 (3.25%)	VUM	VOI <i>Monitored under XBB.1.5-like^c</i>
XBB.1.9.2	313 (0.52%)	VUM	VOI <i>Monitored under XBB.1.5-like^c</i>
XBB.2.3	4,744 (7.98%)	VUM	VOI <i>Monitored under XBB.1.5-like^c</i>

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ADD-23	1,114 (200/21)	VUM	NUMBER UNDER ADD-1.3-21
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aIncludes all descendant lineages (e.g. BA.2.75 counts indicated in the table comprise of all its sublineages, including BN.1 and CH.1.1 cases)
bTotal number of samples with assigned lineages
cSARS-CoV-2 lineages that have similar Spike protein profiles and are characterized by a specific set of mutations (S:Q183E, S:F486P and S:F490S) are monitored under XBB.1.5-like by ECDC. This umbrella includes lineages such as XBB.1.9.1, XBB.1.9.2, and XBB.2.3. For the full list of lineages, please refer to the [ECDC website](#).
dSARS-CoV-2 lineages that have similar Spike protein profiles and are characterized by a specific set of mutations (S:F456L, S:Q183E, S:F486P and S:F490S) are monitored under XBB.1.5-like + F456L by ECDC. This umbrella includes lineages such as EG.5. For the full list of lineages, please refer to the [ECDC website](#).

NOTES (Following WHO definition as of 15 March 2023)

- Variant of interest (VOI)** - A SARS-CoV-2 variant with genetic changes that are predicted or known to affect variant characteristics (e.g. transmissibility, antibody evasion, virulence). Identified to have a growth advantage over other circulating variants in more than one WHO region showing an increasing prevalence and number of cases over time or other epidemiological impacts that suggest an emerging risk to global public health.
- Variant Under Monitoring (VUM)** - A SARS-CoV-2 variant with genetic changes that are suspected to affect virus characteristics and early signals of growth advantage relative to other circulating variants. Epidemiological impact remains unclear and additional monitoring is required to reassess risk of the variant.
- Variant of Concern (VOC)** - Meets the definition of a VOI (see no. 1) and meets at least one of the following criteria, when compared to other variants:
 - Detrimental change in clinical disease severity; OR
 - Change in COVID-19 epidemiology causing substantial impact on the ability of health systems to provide care to COVID-19 patients or other illnesses, thus, requiring major public health interventions; OR
 - Significant decrease in effectiveness of available vaccines in protecting against severe disease.

The variants XBB.1.5 (a sublineage of XBB), XBB.1.16 (a sublineage of XBB), and EG.5 (a sublineage of XBB.1.9.2) are variants of Interest (VOI) identified by the WHO. Variants under monitoring (VUM) include XBB, XBB.1.9.1 (a sublineage of XBB), XBB.1.9.2 (a sublineage of XBB), and XBB.2.3 (a sublineage of XBB). Meanwhile, based on the ECDC, the variants BA.2.75, XBB.1.5-like, and XBB.1.5-like + F456L are classified as VOIs (including EG.5, XBB.1.9.1, XBB.1.9.2, and XBB.2.3).

The World Health Organization (WHO) and the European Centre for Disease Prevention and Control (ECDC) classified BA.2.86, previously under the Variant Under Monitoring (VUM) list, as a Variant of Interest (VOI) last November 21 and 24, respectively. As of the current date, the variant has not yet been detected in the Philippines.

Meanwhile, as of 1 December 2023, XBB.1.16 (a sublineage of XBB) has been removed from the list of VUMs being tracked by the ECDC. While the ECDC has not issued a statement on the delisting of the variant as a VUM, a possible reason for this could be a decrease in the global prevalence of the said variant. For tracking purposes, de-escalated variants will continue to be locally monitored by the Department of Health.

Table 2. Distribution of recently sequenced samples by the Research Institute for Tropical Medicine (RITM), the Southern Philippines Medical Center (SPMC), and the University of the Philippines - Philippine Genome Center (UP-PGC) Visayas released last November 22 - December 1, 2023.

Region	Omicron						Total
	XBB				Other sublineages	Total	
	XBB.1.5	XBB.1.16	XBB.1.9.1	XBB.2.3			
6	2	1	0	22	0	25	25
11	0	0	1	7	2	10	10
NCR	0	0	0	1	0	1	1
Total	2	1	1	30	2	36	36

NOTE: Variants reported above include their own descendant lineages. Case counts per variant may change over time due to the continuous updates in the PANGO tool (lineage assigning application).

Out of the recent 36 samples sequenced by the RITM, SPMC, and the UP-PGC Visayas last November 22 - December 1, 2023: 34 (94.44%) were classified as XBB (including two XBB.1.5 cases, 30 XBB.2.3 cases, and one case each of XBB.1.16 and XBB.1.9.1) and two (5.56%) were classified as other Omicron sublineages.

All detected XBB subvariant cases were local cases from Regions 6, 11, and NCR. Please note that the results above must be interpreted with caution since this is primarily affected by sampling biases and other factors such as logistical issues encountered.

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Note: For additional references and information on the COVID-19 variants you can access the links below:

European Centre for Disease Prevention and Control (ECDC):

[European Centre for Disease Prevention and Control - SARS-CoV-2 variants of concern](#)

World Health Organization Monitoring:

[World Health Organization - Tracking SARS-CoV-2 variants](#)

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